




□1: BAA91568. unnamed protein p...[gi:7022355] BLink, Nucleotide, Related Sequences, Taxonomy, LinkOut

LOCUS BAA91568 634 aa linear PRI 22-FEB-2000
DEFINITION unnamed protein product [Homo sapiens].
ACCESSION BAA91568
PID g7022355
VERSION BAA91568.1 GI:7022355
DBSOURCE locus AK001230 accession [AK001230.1](#)
KEYWORDS.
SOURCE human.
ORGANISM [Homo sapiens](#) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H., Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished (2000)
REFERENCE 2 (residues 1 to 634)
AUTHORS Isogai,T. and Otsuki,T.
TITLE Direct Submission
JOURNAL Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)
COMMENT NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
FEATURES
source Location/Qualifiers
1..634
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RM2001544"
/cell_line="NT2"
/cell_type="teratocarcinoma"
/clone_lib="NT2RM2"
/note="cloning vector: pME18SFL3; mRNA from uninduced NT2 neuronal precursor cells."
Protein
1..634
/name="unnamed protein product"
CDS
1..634
/coded_by="AK001230.1:24..1928"
ORIGIN
1 mslvpatnyi ytplnqlkgg tivnvygvvk ffkppylskg tdycsvvtiv dqtnvkltcl
61 lfsqnyealp iiykngdivr fhrlkiqvky ketqgitssg fasltfegtl gapiiprtss

121 kyfnfttedh kmvealrvwa sthmspswtl lklcdvqpmq yfdltcqllg kaevdgasfl
181 lkvwdgtrtp fpswrqliqd lvlegdlshi hrlqnltidi lvydnvhvha rslkvgsflr
241 iyslhtklqs mnsenqtmis lefhlhggt snyrgirvlpe snsdvdqkk dlesanltan
301 qhsdvcicqse pddsfpssgs vslyevercq qlsatiltdh qylertplca ilkqkapqqy
361 riraklrskk prrlfqsvkl hcwkchllqe vphegldii fqdgatktpv vklqntslyd
421 skiwttknqk grkvavhfvk nngilplsne clllieggtl seicklsnkf nsvipvrsgh
481 edlelldlsa pfliqgtihh ygckqcslr signlnslvd ktswipssva ealgvplqy
541 vfvmtftldd gtgvleaylm dsdkffqipa sevlmdddq ksvdmimdmf cpgikiday
601 pwlecfiksy nvtngtdnqi cyqifdtva edvi
//

Revised: October 24, 2001.

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Comparison

W1

SEQ ID NO; 13

Query Match	99.8%; Score 3317; DB 4; Length 634;
Best Local Similarity	99.8%; Pred. No. 4.2e-265;
Matches	633; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	1 MSLVPATNYIYTPLNQLKGGTIVNVYGVVKFFKPPYLSKGTDYCSVVTIVDQTNVKLTCL 60
Db	1 MSLVPATNYIYTPLNQLKGGTIVNVYGVVKFFKPPYLSKGTDYCSVVTIVDQTNVKLTCL 60
Qy	61 LFSGNYEALPIIYKNGDIVRFHRLKIQVYKKETQGITSSGFASLTATEGTLGAPIIPRTSS 120
Db	61 LFSGNYEALPIIYKNGDIVRFHRLKIQVYKKETQGITSSGFASLTATEGTLGAPIIPRTSS 120
Qy	121 KYFNFTTEDHKMVEALRVWASTHMSPSWTLLKLCDVQPMQYFDLTCQLLGKAEVVGASFL 180
Db	121 KYFNFTTEDHKMVEALRVWASTHMSPSWTLLKLCDVQPMQYFDLTCQLLGKAEVVGASFL 180
Qy	181 LKVWDGTRTPFPSSWRVLIQDVLVLEGDLSHIHRLQNLNTIDILVYDNHVHVARSLKVGSLR 240
Db	181 LKVWDGTRTPFPSSWRVLIQDVLVLEGDLSHIHRLQNLNTIDILVYDNHVHVARSLKVGSLR 240
Qy	241 IYSLHTKLQSMNSENQTMLSLEFHLLHGCTS YGRGIRVLPESNSDVLKDDLESANLTAN 300
Db	241 IYSLHTKLQSMNSENQTMLSLEFHLLHGCTS YGRGIRVLPESNSDVLKDDLESANLTAN 300
Qy	301 QHSDVICQSEPDSSFPSSGSVSLYEVERCQQLSATILTDXQYLERTPLCAILKQKAPQQY 360
Db	301 QHSDVICQSEPDSSFPSSGSVSLYEVERCQQLSATILTDXQYLERTPLCAILKQKAPQQY 360
Qy	361 RIRAKLRSYKPRRLFQSVKLHC PKCHLLQEVPHEGDLDII FQDGATKTPVVKLQNTSLYD 420
Db	361 RIRAKLRSYKPRRLFQSVKLHC PKCHLLQEVPHEGDLDII FQDGATKTPVVKLQNTSLYD 420
Qy	421 SKIWTTKNQKGRKVAHFVKNNGILPLSNECLLIEGGTLSEICKLSNKFNSVIPVRSGH 480
Db	421 SKIWTTKNQKGRKVAHFVKNNGILPLSNECLLIEGGTLSEICKLSNKFNSVIPVRSGH 480
Qy	481 EDLELLDLSAPFLIQGTIHGYGCKCSSLRSIQNLNSLVDKTSWIPSSVAEALGIVPLQY 540
Db	481 EDLELLDLSAPFLIQGTIHGYGCKCSSLRSIQNLNSLVDKTSWIPSSVAEALGIVPLQY 540
Qy	541 VFVMTFTLDDGTGVLEAYLMDSDKFQIPASEVLMDDDLQKSVDMMIMDMFCPPGIKIDAY 600
Db	541 VFVMTFTLDDGTGVLEAYLMDSDKFQIPASEVLMDDDLQKSVDMMIMDMFCPPGIKIDAY 600
Qy	601 PWLECFIKSYNVTNGTDNQICYQIFDTTVAEDVI 634
Db	601 PWLECFIKSYNVTNGTDNQICYQIFDTTVAEDVI 634

RESULT 3

Wed Apr 10 08:35:23 2002

us-09-81

Comparison
SEQIDNO:17

	Matches	503;	Conservative	1;	Mismatches	3;	Indels	0;	Gaps	0;
Qy	1	MSLVPATNYIYTPLNQLKGGTIVNVYGVVKFFKPPYLSKGTDYCSVVTIVDQTNVKLTCL	60							
Db	1	MSLVPATNYIYTPLNQLKGGTIVNVYGVVKFFKPPYLSKGTDYCSVVTIVDQTNVKLTCL	60							
Qy	61	LFGSNYEALPIIYKNGDIVRFHRLKIQVYKKE	TQGITSSGFA	SALT	FEGTLGAPIIPRTSS	120				
Db	61	LFGSNYEALPIIYKNGDIVRFHRLKIQVYKKE	TQGITSSGFA	SALT	FEGTLGAPIIPRTSS	120				
Qy	121	KYFNFTTEDHKMVEALRVWASTHMSPSW	TLLKLCDVQPMQYFDLTCQ	LLGKAEV	DGASFL	180				
Db	121	KYFNFTTEDHKMVEALRVWASTHMSPSW	TLLKLCDVQPMQYFDLTCQ	LLGKAEV	DGASFL	180				
Qy	181	LKVWDGTRTPFP	SWRVLIQDVL	LEGDL	SHIHRQLNLTIDILVYDNHV	VARSILKVGSLR	240			
Db	181	LKVWDGTRTPFP	SWRVLIQDVL	LEGDL	SHIHRQLNLTIDILVYDNHV	VARSILKVGSLR	240			
Qy	241	IYSLHTKLQSMNSE	NQMLSLE	FHLHGGS	TSYGRGIRVLPESNSD	VQYFDLCKKDLESANLTAN	300			
Db	241	IYSLHTKLQSMNSE	NQMLSLE	FHLHGGS	TSYGRGIRVLPESNSD	VQYFDLCKKDLESANLTAN	300			
Qy	301	QHSDVICQSEPD	DSFPSSGSV	SLYEVERCQQLSATIL	TDHQYLER	PLCAILKQKAPQQY	360			
Db	301	QHSDVICQSEPD	DSFPSSGSV	SLYEVERCQQLSATIL	TDHQYLER	PLCAILKQKAPQQY	360			
Qy	361	RIRAKLRSYKPRRLF	QSVKLHCPKCHLLQE	VPHEGDLDII	FQDGATKTPDV	QLQNTSLYD	420			
Db	361	RIRAKLRSYKPRRLF	QSVKLHCPKCHLLQE	VPHEGDLDII	FQDGATKTPDV	QLQNTSLYD	420			
Qy	421	SKIWTTKNQKGRKVA	HFKVNN	GILPLSNEC	LIEGGTL	SEICKLSNKFNSVIPVRSGH	480			
Db	421	SKIWTTKNQKGRKVA	HFKVNN	GILPLSNEC	LIEGGTL	SEICKLSNKFNSVIPVRSGH	480			
Qy	481	EDLELLDLSAPFLIQGT	TIHHYGTGYCT				507			
Db	481	EDLELLDLSAPFLIQGT	TIHHYGTGYCT				507			

Comparison: SEQ ID NO: 15

Query Match 93.5%; Score 1660; DB 4; Length 634;
 Best Local Similarity 98.8%; Pred. No. 1e-138;
 Matches 317; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Query 1 MSLVPAATNYTPIQNLKGQTIVWVGVVKFPPVLSKGTYCSVUTIVDQVVKTC
 Db 1 MSLVPAATNYTPIQNLKGQTIVWVGVVKFPPVLSKGTYCSVUTIVDQVVKTC 60
 Query 61 LPSQNYEALPIIKNGDIVRFRKLICKVYKKTQGTTGGTCAPIIPRTSS 60
 Db 61 LPSQNYEALPIIKNGDIVRFRKLICKVYKKTQGTTGGTCAPIIPRTSS 120
 Query 121 KFNFTTEDHKAVEARWASHMSPSWTLKLCDVQPMOYFDLTCOLIGKAEYGASFL 120
 Db 121 KFNFTTEDHKAVEARWASHMSPSWTLKLCDVQPMOYFDLTCOLIGKAEYGASFL 180
 Query 181 LKVMDGTRTPPSWRVLIQDWLEGDLSHIRLQLMFLIDLYDHWHTARSKVGSFLR 180
 Db 181 LKVMDGTRTPPSWRVLIQDWLEGDLSHIRLQLMFLIDLYDHWHTARSKVGSFLR 240

Qy	241	ISLHFKLQSMNSENQNTM SLEFHHLGAGSYGRCIRVLPESENSDVDOOKKOLESANLTAN
Db	241	
Qy	301	QHSVTICQSEPDDSPFNGVSL 321
Db	301	: :
		QHSVICQSEPDDSPFNGSV 321